Claims

It is claimed:

1.   A method for determining the presence or absence of a target biochemical or biochemical complex in a sample, comprising:

(i)   receiving mobility data from an analysis of one or more released mobility probes using a mobility dependent analysis technique;

(ii)   extracting at least one feature or feature set from the mobility data;

(iii)   receiving information for associating the at least one feature or feature set to the one or more released mobility probes;

(iv)   associating one of the one or more released mobility probes with a respective target biochemical or biochemical complex; and

(v)   determining the presence or absence of the target biochemical or biochemical complex.

2.   The method of claim 1, further comprising:

reporting the presence or absence of the target biochemical or biochemical complex.

3.   The method of claim 1, wherein the mobility dependent analysis technique comprises electrophoresis.

4.   The method of claim 1, wherein the target biochemical or biochemical complex comprises a nucleic acid, protein, or peptide.

5.   The method of claim 1, wherein the target biochemical or biochemical complex comprises a single nucleotide polymorphism.

6.   The method of claim 5, wherein the at least one feature or feature set comprises a plurality of peaks, and further wherein the step of determining the presence or absence of the target biochemical or biochemical complex comprises:

computing a ratio of smallest peak height to largest peak height for a set of two peaks associated with the single nucleotide polymorphism; and

calling the single nucleotide polymorphism heterozygous if the ratio is greater than a selected threshold.

7.   The method of claim 5, wherein the determination of the presence or absence of a target biochemical or biochemical complex includes utilization of a clustering technique.

8.   A method for determining the presence or absence of a target biochemical or biochemical complex in a sample, comprising:

(i)   receiving mobility data from an analysis of a plurality of released mobility probes using a mobility dependent analysis technique;

(ii)   extracting a feature set from the mobility data;

(iii)   receiving information for associating the feature set to the plurality of released mobility probes;

(iv)   associating a released mobility probe with a respective target biochemical or biochemical complex;

(v)   determining the presence or absence of the target biochemical or biochemical complex.

9.   The method of claim 8, further comprising:

reporting the presence or absence of the target biochemical or biochemical complex.

10.   The method of claim 8, further comprising:

entering the presence or absence of the target biochemical or biochemical complex into a database.

11.   A program storage device readable by a machine, embodying a program of instructions executable by the machine to perform method steps for analysis of a target biochemical or biochemical complex in a sample, said method steps comprising:

(i)   receiving mobility data from an analysis of one or more released mobility probes using a mobility dependent analysis technique;

(ii)   extracting at least one feature or feature set from the mobility data;

(iii)   receiving information for associating the at least one feature or feature set to the one or more released mobility probes;

(iv)   associating one of the one or more released mobility probes with a respective target biochemical or biochemical complex; and

(v)   determining the presence or absence of the target biochemical or biochemical complex.

12.   The device of claim 11, wherein said method steps further comprise:

reporting the presence or absence of the target biochemical or biochemical complex.

13.   The device of claim 11, wherein said method steps further comprise:

entering the presence or absence of the target biochemical or biochemical complex in a database.

14.   A method for genetic analysis, comprising:

analyzing a plurality of samples on an electrophoresis instrument, with each sample representing an individual of a population, whereby mobility data is generated for each sample;

receiving said mobility data, represented as fluorescence intensity over time;

associating the mobility data with the presence or absence of one or more target biochemicals or biochemical complexes in the samples;

transforming the mobility data to a different feature space;

assigning a class to each sample based on said transforming; and

determining a genoptypic characteristic of each sample or the population based the class assignment.

15.   The method of claim 14, wherein the step of transforming the data to a different feature space includes transformation to rho theta coordinates.

16.   The method of claim 14, wherein the step of assigning a class to each sample includes utilization of a clustering technique.

17.   A program storage device readable by a machine, embodying a program of instructions executable by the machine to perform genetic analysis, said method steps comprising:

receiving mobility data, represented as fluorescence intensity over time, generated by electrophoresis of a plurality of samples, with each sample representing an individual of a population;

associating the mobility data with the presence or absence of one or more target biochemicals or biochemical complexes in the samples;

transforming the mobility data to a different feature space; and

assigning a class to each sample based on said transforming.

18.   The device of claim 17, wherein said method steps further comprise:

determining a genoptypic characteristic of each sample or the population based the class assignment.

19.   A method for determining a target biochemical or biochemical complex, comprising:

(i)   receiving mobility-dependent data representing the output of a mobility-dependent analysis technique;

(ii)   receiving data for associating the mobility-dependent data with a mobility probe;

(iii)   receiving data for associating the mobility probe with a tag or a complimentary tag sequence;

(iv)   receiving data for associating the tag or complimentary tag sequence with a target;

and, using the data from (ii), (iii), and (iv):

(v)   associating the mobility-dependent data with a corresponding mobility probe;

(vi)   associating the mobility probe from (v) with a corresponding tag or complimentary tag sequence;

(vii)   associating the tag or complimentary tag sequence from (vi) with a corresponding target; and

(viii)   reporting the detection of the target from (vii).

20.   The method of claim 19, wherein steps (i) through (viii) are performed two or more times, in a serial fashion.

21.   The method of claim 19, wherein steps (i) through (viii) are performed two or more times, in a parallel fashion.

22.   A method for determining a target biochemical or biochemical complex, comprising:

(i)   receiving mobility-dependent data representing the output of a mobility-dependent analysis technique;

(ii)   receiving data for associating the mobility-dependent data with a plurality of mobility probes;

(iii)   receiving data for associating each of the mobility probes with a respective tag or complimentary tag sequence;

(iv)   receiving data for associating the tag or complimentary tag sequence from (iii) with a respective target;

and, using the data from (ii), (iii), and (iv):

(v)   associating the mobility-dependent data with the plurality of mobility probes;

(vi)   associating each of the plurality of mobility probes with a corresponding tag or complimentary tag sequence;

(vii)   associating each tag or complimentary tag sequence from (vi) with a corresponding target; and

(viii)   reporting the detection of each target from (vii).

23.   The method of claim 22, wherein step (viii) includes entering the detection of each target into a database.

24.   A program storage device readable by a machine, embodying a program of instructions executable by the machine for determining a target biochemical or biochemical complex, said method steps comprising:

(i)   receiving mobility-dependent data representing the output of a mobility-dependent analysis technique;

(ii)   receiving data for associating the mobility-dependent data with a mobility probe;

(iii)   receiving data for associating the mobility probe with a tag or a complimentary tag sequence;

(iv)   receiving data for associating the tag or complimentary tag sequence with a target;

and, using the data from (ii), (iii), and (iv):

(v)   associating the mobility-dependent data with a corresponding mobility probe;

(vi)　　associating the mobility probe from (v) with a corresponding tag or complimentary tag sequence;

(vii)　　associating the tag or complimentary tag sequence from (vi) with a corresponding target; and

(viii)　　reporting the detection of the target from (vii).

25.　　A program storage device readable by a machine, embodying a program of instructions executable by the machine for determining one or more target biochemicals or biochemical complexes, said method steps comprising:

(i)　　receiving mobility-dependent data representing the output of a mobility-dependent analysis technique;

(ii)　　receiving data for associating the mobility-dependent data with a plurality of mobility probes;

(iii)　　receiving data for associating each of the plurality of mobility probes with a respective target biochemical or biochemical complex;

and, using the data from (ii) and (iii):

(iv)　　associating the mobility-dependent data with the mobility probes;

(v)　　associating each of the mobility probes from (iv) with a corresponding target; and

(vi)　　reporting the detection of the target from (v).

26.　　The device of claim 25, wherein the mobility probes are released mobility probes.

27.　　A method for genetic analysis, comprising:

receiving electropherogram data;

extracting peaks from the electropherogram data;

associating the peaks with respective released mobility probes;

associating the released mobility probes with respective targets;

analyzing the peaks against selected criteria to filter out peaks not indicative of targets; and

reporting the detection of targets.